

PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/744,125

DATE: 10/26/2001

TIME: 15:05:43

Input Set : A:\st98045sqli.txt

Output Set: N:\CRF3\10262001\I744125.raw

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3 <110> APPLICANT: MARCIREAU, Christophe
4     MULTON, Marie-Christine
5     POLARD-HOuset, Valerie
7 <120> TITLE OF INVENTION: MEKK1-INTERACTING FHA PROTEIN (M1F1)
9 <130> FILE REFERENCE: A3233A US
11 <140> CURRENT APPLICATION NUMBER: 09/744,125
12 <141> CURRENT FILING DATE: 2001-01-19
14 <150> PRIOR APPLICATION NUMBER: PCT/EP99/05142
15 <151> PRIOR FILING DATE: 1999-07-21
17 <150> PRIOR APPLICATION NUMBER: US 60/093,590
18 <151> PRIOR FILING DATE: 1998-07-21
20 <160> NUMBER OF SEQ ID NOS: 15
22 <170> SOFTWARE: PatentIn version 3.0
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25 <211> LENGTH: 2973
26 <212> TYPE: DNA
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44 gtgtgtaagg ctgtaaagcc caatctgcag gtgttgcgag cccgattctc tgagatcaca    480
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48 gctgtggatg tgaggcagga gctggacctg aggattggag ctgcctttac taggttccag    600
50 accctgcggc ttcagaggat ttttcttgag gtgctggcag agcagctcat cagttacggc    660
52 agctgccagt tccccacact gggctttgtg gtggagcggg tcaaagccat tcaggctttt    720
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56 ttcaactgga aaaggcatcg actctttaac cacacggctt gcctagtctc ctatcagttg    840
58 tgtgtggagg atcccatggc aactgtggta gaggtcagat ctaagcccaa gagcaagtgg    900
60 cggcctcaag ccttggacac tgtggagcct gagaagctgg cttctcgaaa gttgagaata    960
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84 cacctgggca tgggacttgt ggaaggttat gattccatgg gctatgaaat gtctaagcct   1680
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88 tttgtggttc taaggcagca agtgcagaaa tacaagcagg ttttcattga agcgggtggct 1800
90 aaagcaaaga aattggacga ggccttgccc cagtactttg ggaatgggac agagttggcc 1860
92 cagcaagaag atatctaccc agccatgccg gagcccatca ggaagtggcc acagtgcac 1920
94 aaggacatgg tccttaagac caagaagaat ggcggttctt acctcagctg catgggtttc 1980
96 ccagagtgtc gctcagctgt gtggcttctt gactcgggtg tggaggccag cagggacagc 2040
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114 gcatatagac ccctgggcgc ctccctggga tgcccaccag gcccagggat ccacctaggt 2580
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131 &lt;210&gt; SEQ ID NO: 2

132 &lt;211&gt; LENGTH: 974

133 &lt;212&gt; TYPE: PRT

134 &lt;213&gt; ORGANISM: Homo sapiens

136 &lt;400&gt; SEQUENCE: 2

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139 1 5 10 15
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142 20 25 30
144 Arg Arg Glu Gly Leu Ser Lys Phe Asn Lys Ile Tyr Glu Phe Asp Tyr
145 35 40 45
147 His Leu Tyr Gly Gln Asn Val Thr Met Val Met Thr Ser Val Ser Gly
148 50 55 60
150 His Leu Leu Ala His Asp Phe Gln Met Gln Phe Arg Lys Trp Gln Ser
151 65 70 75 80
153 Cys Asn Pro Leu Val Leu Phe Glu Ala Glu Ile Glu Lys Tyr Cys Pro
154 85 90 95
156 Glu Asn Phe Val Asp Ile Lys Lys Thr Leu Glu Arg Glu Thr Arg Gln
157 100 105 110
159 Cys Gln Ala Leu Val Ile Trp Thr Asp Cys Asp Arg Glu Gly Glu Asn
160 115 120 125
162 Ile Gly Phe Glu Ile Ile His Val Cys Lys Ala Val Lys Pro Asn Leu
163 130 135 140
165 Gln Val Leu Arg Ala Arg Phe Ser Glu Ile Thr Pro His Ala Val Arg
166 145 150 155 160
168 Thr Ala Cys Glu Asn Leu Thr Glu Pro Asp Gln Arg Val Ser Asp Ala
169 165 170 175
171 Val Asp Val Arg Gln Glu Leu Asp Leu Arg Ile Gly Ala Ala Phe Thr

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Input Set : A:\st98045sqli.txt

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174	Arg Phe Gln Thr Leu Arg Leu Gln Arg Ile Phe Pro Glu Val Leu Ala					
175		195		200		205
177	Glu Gln Leu Ile Ser Tyr Gly Ser Cys Gln Phe Pro Thr Leu Gly Phe					
178		210		215		220
180	Val Val Glu Arg Phe Lys Ala Ile Gln Ala Phe Val Pro Glu Ile Phe					
181	225		230		235	240
183	His Arg Ile Lys Val Thr His Asp His Lys Asp Gly Ile Val Glu Phe					
184		245		250		255
186	Asn Trp Lys Arg His Arg Leu Phe Asn His Thr Ala Cys Leu Val Leu					
187		260		265		270
189	Tyr Gln Leu Cys Val Glu Asp Pro Met Ala Thr Val Val Glu Val Arg					
190		275		280		285
192	Ser Lys Pro Lys Ser Lys Trp Arg Pro Gln Ala Leu Asp Thr Val Glu					
193		290		295		300
195	Leu Glu Lys Leu Ala Ser Arg Lys Leu Arg Ile Asn Ala Lys Glu Thr					
196	305		310		315	320
198	Met Arg Ile Ala Glu Lys Leu Tyr Thr Gln Gly Tyr Ile Ser Tyr Pro					
199		325		330		335
201	Arg Thr Glu Thr Asn Ile Phe Pro Arg Asp Leu Asn Leu Thr Val Leu					
202		340		345		350
204	Val Glu Gln Gln Thr Pro Asp Pro Arg Trp Gly Ala Phe Ala Gln Ser					
205		355		360		365
207	Ile Leu Glu Arg Gly Gly Pro Thr Pro Arg Asn Gly Asn Lys Ser Asp					
208		370		375		380
210	Gln Ala His Pro Pro Ile His Pro Thr Lys Tyr Thr Asn Asn Leu Gln					
211	385		390		395	400
213	Gly Asp Glu Gln Arg Leu Tyr Glu Phe Ile Val Arg His Phe Leu Ala					
214		405		410		415
216	Cys Cys Ser Gln Asp Ala Gln Gly Gln Glu Thr Thr Val Glu Ile Asp					
217		420		425		430
219	Ile Ala Gln Glu Arg Phe Val Ala His Gly Leu Met Ile Leu Ala Arg					
220		435		440		445
222	Asn Tyr Leu Asp Val Tyr Pro Tyr Asp His Trp Ser Asp Lys Ile Leu					
223		450		455		460
225	Pro Val Tyr Glu Gln Gly Ser His Phe Gln Pro Ser Thr Val Glu Met					
226	465		470		475	480
228	Val Asp Gly Glu Thr Ser Pro Pro Lys Leu Leu Thr Glu Ala Asp Leu					
229		485		490		495
231	Ile Ala Leu Met Glu Lys His Gly Ile Gly Thr Asp Ala Thr His Ala					
232		500		505		510
234	Glu His Ile Glu Thr Ile Lys Ala Arg Met Tyr Val Gly Leu Thr Pro					
235		515		520		525
237	Asp Lys Arg Phe Leu Pro Gly His Leu Gly Met Gly Leu Val Glu Gly					
238		530		535		540
240	Tyr Asp Ser Met Gly Tyr Glu Met Ser Lys Pro Asp Leu Arg Ala Glu					
241	545		550		555	560
243	Leu Glu Ala Asp Leu Lys Leu Ile Cys Asp Gly Lys Lys Asp Lys Phe					
244		565		570		575

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246 Val Val Leu Arg Gln Gln Val Gln Lys Tyr Lys Gln Val Phe Ile Glu
247      580      585      590
249 Ala Val Ala Lys Ala Lys Lys Leu Asp Glu Ala Leu Ala Gln Tyr Phe
250      595      600      605
252 Gly Asn Gly Thr Glu Leu Ala Gln Gln Glu Asp Ile Tyr Pro Ala Met
253      610      615      620
255 Pro Glu Pro Ile Arg Lys Cys Pro Gln Cys Asn Lys Asp Met Val Leu
256 625      630      635      640
258 Lys Thr Lys Lys Asn Gly Gly Phe Tyr Leu Ser Cys Met Gly Phe Pro
259      645      650      655
261 Glu Cys Arg Ser Ala Val Trp Leu Pro Asp Ser Val Leu Glu Ala Ser
262      660      665      670
264 Arg Asp Ser Ser Val Cys Pro Val Cys Gln Pro His Pro Val Tyr Arg
265      675      680      685
267 Leu Lys Leu Lys Phe Lys Arg Gly Ser Leu Pro Pro Thr Met Pro Leu
268      690      695      700
270 Glu Phe Val Cys Cys Ile Gly Gly Cys Asp Asp Thr Leu Arg Glu Ile
271 705      710      715      720
273 Leu Asp Leu Arg Phe Ser Gly Gly Pro Pro Arg Ala Ser Gln Pro Ser
274      725      730      735
276 Gly Arg Leu Gln Ala Asn Gln Ser Leu Asn Arg Met Asp Asn Ser Gln
277      740      745      750
279 His Pro Gln Pro Ala Asp Ser Arg Gln Thr Gly Ser Ser Lys Ala Leu
280      755      760      765
282 Ala Gln Thr Leu Pro Pro Pro Thr Ala Ala Gly Glu Ser Asn Ser Val
283      770      775      780
285 Thr Cys Asn Cys Gly Gln Glu Ala Val Leu Leu Thr Val Arg Lys Glu
286 785      790      795      800
288 Gly Pro Asn Arg Gly Arg Gln Phe Phe Lys Cys Asn Gly Gly Ser Cys
289      805      810      815
291 Asn Phe Phe Leu Trp Ala Asp Ser Pro Asn Pro Gly Ala Gly Gly Pro
292      820      825      830
294 Pro Ala Leu Ala Tyr Arg Pro Leu Gly Ala Ser Leu Gly Cys Pro Pro
295      835      840      845
297 Gly Pro Gly Ile His Leu Gly Gly Phe Gly Asn Pro Gly Asp Gly Ser
298      850      855      860
300 Gly Ser Gly Thr Ser Cys Leu Cys Ser Gln Pro Ser Val Thr Arg Thr
301 865      870      875      880
303 Val Gln Lys Asp Gly Pro Asn Lys Gly Arg Gln Phe His Thr Cys Ala
304      885      890      895
306 Lys Pro Arg Glu Gln Gln Cys Gly Phe Phe Gln Trp Val Asp Glu Asn
307      900      905      910
309 Thr Ala Pro Gly Thr Ser Gly Ala Pro Ser Trp Thr Gly Asp Arg Gly
310      915      920      925
312 Arg Thr Leu Glu Ser Glu Ala Arg Ser Lys Arg Pro Arg Ala Ser Ser
313      930      935      940
315 Ser Asp Met Gly Ser Thr Ala Lys Lys Pro Arg Lys Cys Ser Leu Cys
316 945      950      955      960
318 His Gln Pro Gly His Thr Arg Pro Phe Cys Pro Gln Asn Arg

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TIME: 15:05:43

Input Set : A:\st98045sqli.txt

Output Set: N:\CRF3\10262001\I744125.raw

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324 <213> ORGANISM: Homo sapiens
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331 gagcctcaga ttcgtagaat agtcgaacaa gatactatgc ctccaaaggg tgtccgccac    180
333 actatgatgt ttagtgctac ttttcctaag gaaatacaga tgctggctcg tgatttctta    240
335 gatgaatata tcttcttggc tgtaggaaga gttggctcta cctctgaaaa catcacacag    300
337 aaagtagttt gggtagaaga atcagacaaa cggtcatttc tgcttgacct cctaaatgca    360
339 acaggcaagg attcactgac cttagtgttt gtggagacca aaaaggggtgc agattctctg    420
341 gaggatttct tataccatga aggatacgca tgtaccagca tccatggaga ccgttctcag    480
343 agggatagag aagaggccct tcaccagttc cgctcaggaa aaagcccaat tttagtggct    540
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347 ttgccaagtg atattgaaga atatgtacat cgtattggtc gtacgggacg ttaggaaac    660
349 cttggcctgg caacctcatt ctttaacgag aggaacataa atattactaa ggatttggtg    720
351 gatcttcttg ttgaagctaa acaagaagtg ccgtcttggt tagaaaacat ggcttatgaa    780
353 caccactaca agggtagcag tcgtggacgt tctaagagca gatttagtgg agggtttggt    840
355 gccagagact accgacaaag tagcggtgcc agcagttcca gcttcagcag cagccgcgca    900
357 agcagcagcc gcagtggcgg aggtggccac ggtagcagca gaggatttgg tggaggtggc    960
359 tatggaggct tttaacaacag tgatggata ggaggaaatt ataactcca ggggggttgac   1020
361 tgggtgggta actgagcctg ctttgca ggtcaccctg ccaaacaagc taatatggaa   1080
363 accacatgta acttagccag actatacctt gtgtagcttc aagaactcgc agtacattac   1140
365 cagctgtgat tctccactga aatttttttt ttaagggagc tcaaggtcac aagaagaaat   1200
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373 <213> ORGANISM: Homo sapiens
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381                20                      25                      30
383 Asp Arg Met Leu Asp Met Gly Phe Glu Pro Gln Ile Arg Arg Ile Val
384                35                      40                      45
386 Glu Gln Asp Thr Met Pro Pro Lys Gly Val Arg His Thr Met Met Phe
387                50                      55                      60
389 Ser Ala Thr Phe Pro Lys Glu Ile Gln Met Leu Ala Arg Asp Phe Leu
390 65                      70                      75                      80
392 Asp Glu Tyr Ile Phe Leu Ala Val Gly Arg Val Gly Ser Thr Ser Glu
393                85                      90                      95
395 Asn Ile Thr Gln Lys Val Val Trp Val Glu Glu Ser Asp Lys Arg Ser
396                100                     105                     110
398 Phe Leu Leu Asp Leu Leu Asn Ala Thr Gly Lys Asp Ser Leu Thr Leu
399                115                     120                     125
401 Val Phe Val Glu Thr Lys Lys Gly Ala Asp Ser Leu Glu Asp Phe Leu

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## VERIFICATION SUMMARY

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Input Set : A:\st98045sqli.txt

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L:788 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
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